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Sequence Listing was accepted with existing errors.

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Reviewer: Keisha Douglas

Timestamp: Thu Jul 19 16:46:16 EDT 2007

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Application No: 10633484 Version No: 1.1

Input Set:

Output Set:

Started: 2007-07-19 16:45:59.052
Finished: 2007-07-19 16:45:59.920
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 868 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

SEQUENCE LISTING

<110> Rudiger Ridder, et.al.

<120> Method for solution based diagnosis

<130> 05033.0003.00US00

<140> 10/633,484

<141> 2003-07-31

<150> EP 02017313.4

<151> 2002-08-01

<160> 14

<170> PatentIn version 3.3

<210> 1

<211> 745

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(745)

<223> gamma-Catenin, Swissprot Accession Q86W21

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Gln Gln Thr Tyr Thr Tyr Asp Ser Gly Ile His Ser Gly Ala Asn Thr
20 25 30

Cys Val Pro Ser Val Ser Ser Lys Gly Ile Met Glu Glu Asp Glu Ala
35 40 45

Cys Gly Arg Gln Tyr Thr Leu Lys Lys Thr Thr Thr Tyr Thr Gln Gly
50 55 60

Val Pro Pro Ser Gln Gly Asp Leu Glu Tyr Gln Met Ser Thr Thr Ala
65 70 75 80

Arg Ala Lys Arg Val Arg Glu Ala Met Cys Ser Gly Val Ser Gly Glu
85 90 95

Asp Ser Ser Leu Leu Leu Ala Thr Gln Val Glu Gly Gln Ala Thr Asn
100 105 110

Leu Gln Arg Leu Ala Glu Pro Ser Gln Leu Leu Lys Ser Ala Ile Val
115 120 125

His Leu Ile Asn Tyr Gln Asp Asp Ala Glu Leu Ala Thr Arg Ala Leu
130 135 140

Pro Glu Leu Thr Lys Leu Leu Asn Asp Glu Asp Pro Val Val Val Thr
145 150 155 160

Lys Ala Ala Met Ile Val Asn Gln Leu Ser Lys Lys Glu Ala Ser Arg
165 170 175

Arg Ala Leu Met Gly Ser Pro Gln Leu Val Ala Ala Val Val Arg Thr
180 185 190

Met Gln Asn Thr Ser Asp Leu Asp Thr Ala Arg Cys Thr Thr Ser Ile
195 200 205

Leu His Asn Leu Ser His His Arg Glu Gly Leu Leu Ala Ile Phe Lys
210 215 220

Ser Gly Gly Ile Pro Ala Leu Val Arg Met Leu Ser Ser Pro Val Glu
225 230 235 240

Ser Val Leu Phe Tyr Ala Ile Thr Thr Leu His Asn Leu Leu Leu Tyr
245 250 255

Gln Glu Gly Ala Lys Met Ala Val Arg Leu Ala Asp Gly Leu Gln Lys
260 265 270

Met Val Pro Leu Leu Asn Lys Asn Asn Pro Lys Phe Leu Ala Ile Thr
275 280 285

Thr Asp Cys Leu Gln Leu Leu Ala Tyr Gly Asn Gln Glu Ser Lys Leu
290 295 300

Ile Ile Leu Ala Asn Gly Gly Pro Gln Ala Leu Val Gln Ile Met Arg
305 310 315 320

Asn Tyr Ser Tyr Glu Lys Leu Leu Trp Thr Thr Ser Arg Val Leu Lys
325 330 335

Val	Leu	Ser	Val	Cys	Pro	Ser	Asn	Lys	Pro	Ala	Ile	Val	Glu	Ala	Gly	340	345	350	
Gly	Met	Gln	Ala	Leu	Gly	Lys	His	Leu	Thr	Ser	Asn	Ser	Pro	Arg	Leu	355	360	365	
Val	Gln	Asn	Cys	Leu	Trp	Thr	Leu	Arg	Asn	Leu	Ser	Asp	Val	Ala	Thr	370	375	380	
Lys	Gln	Glu	Gly	Leu	Glu	Ser	Val	Leu	Lys	Ile	Leu	Val	Asn	Gln	Leu	385	390	395	400
Ser	Val	Asp	Asp	Val	Asn	Val	Leu	Thr	Cys	Ala	Thr	Gly	Thr	Leu	Ser	405	410	415	
Asn	Leu	Thr	Cys	Asn	Asn	Ser	Lys	Asn	Lys	Thr	Leu	Val	Thr	Gln	Asn	420	425	430	
Ser	Gly	Val	Glu	Ala	Leu	Ile	His	Ala	Ile	Leu	Arg	Ala	Gly	Asp	Lys	435	440	445	
Asp	Asp	Ile	Thr	Glu	Pro	Ala	Val	Cys	Ala	Leu	Arg	His	Leu	Thr	Ser	450	455	460	
Arg	His	Pro	Glu	Ala	Glu	Met	Ala	Gln	Asn	Ser	Val	Arg	Leu	Asn	Tyr	465	470	475	480
Gly	Ile	Pro	Ala	Ile	Val	Lys	Leu	Leu	Asn	Gln	Pro	Asn	Gln	Trp	Pro	485	490	495	
Leu	Val	Lys	Ala	Thr	Ile	Gly	Leu	Ile	Arg	Asn	Leu	Ala	Leu	Cys	Pro	500	505	510	
Ala	Asn	His	Ala	Pro	Leu	Gln	Glu	Ala	Ala	Val	Ile	Pro	Arg	Leu	Val	515	520	525	
Gln	Leu	Leu	Val	Lys	Ala	His	Gln	Asp	Ala	Gln	Arg	His	Val	Ala	Ala	530	535	540	
Gly	Thr	Gln	Gln	Pro	Tyr	Thr	Asp	Gly	Val	Arg	Met	Glu	Glu	Ile	Val	545	550	555	560

Glu Gly Cys Thr Gly Ala Leu His Ile Leu Ala Arg Asp Pro Met Asn
565 570 575

Arg Met Glu Ile Phe Arg Leu Asn Thr Ile Pro Leu Phe Val Gln Leu
580 585 590

Leu Tyr Ser Ser Val Glu Asn Ile Gln Arg Val Ala Ala Gly Val Leu
595 600 605

Cys Glu Leu Ala Gln Asp Lys Glu Ala Ala Asp Ala Ile Asp Ala Glu
610 615 620

Gly Ala Ser Ala Pro Leu Met Glu Leu Leu His Ser Arg Asn Glu Gly
625 630 635 640

Thr Ala Thr Tyr Ala Ala Ala Val Leu Phe Arg Ile Ser Glu Asp Lys
645 650 655

Asn Pro Asp Tyr Arg Lys Arg Val Ser Val Glu Leu Thr Asn Ser Leu
660 665 670

Phe Lys His Asp Pro Ala Ala Trp Glu Ala Ala Gln Ser Met Ile Pro
675 680 685

Ile Asn Glu Pro Tyr Gly Asp Asp Leu Asp Ala Thr Tyr Arg Pro Met
690 695 700

Tyr Ser Ser Asp Val Pro Leu Asp Pro Leu Glu Met His Met Asp Met
705 710 715 720

Asp Gly Asp Tyr Pro Ile Asp Thr Tyr Ser Asp Gly Leu Arg Pro Pro
725 730 735

Tyr Pro Thr Ala Asp His Met Leu Ala
740 745

<210> 2
<211> 314
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(314)

<223> Ep-Cam, Swissprot Accession P16422

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Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser

210

215

220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
 225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
 245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
 260 265 270

Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
 275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
 290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
 305 310

<210> 3
 <211> 882
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(882)
 <223> E-Cadherin, Swissprot Accession P12830

<400> 3

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Val Ser Ser Trp Leu Cys Gln Glu Pro Glu Pro Cys His Pro Gly Phe
 20 25 30

Asp Ala Glu Ser Tyr Thr Phe Thr Val Pro Arg Arg His Leu Glu Arg
 35 40 45

Gly Arg Val Leu Gly Arg Val Asn Phe Glu Asp Cys Thr Gly Arg Gln
 50 55 60

Arg Thr Ala Tyr Phe Ser Leu Asp Thr Arg Phe Lys Val Gly Thr Asp

65		70		75		80									
Gly	Val	Ile	Thr	Val	Lys	Arg	Pro	Leu	Arg	Phe	His	Asn	Pro	Gln	Ile
				85				90						95	
His	Phe	Leu	Val	Tyr	Ala	Trp	Asp	Ser	Thr	Tyr	Arg	Lys	Phe	Ser	Thr
		100						105					110		
Lys	Val	Thr	Leu	Asn	Thr	Val	Gly	His	His	His	Arg	Pro	Pro	Pro	His
		115					120					125			
Gln	Ala	Ser	Val	Ser	Gly	Ile	Gln	Ala	Glu	Leu	Leu	Thr	Phe	Pro	Asn
	130					135						140			
Ser	Ser	Pro	Gly	Leu	Arg	Arg	Gln	Lys	Arg	Asp	Trp	Val	Ile	Pro	Pro
145					150					155					160
Ile	Ser	Cys	Pro	Glu	Asn	Glu	Lys	Gly	Pro	Phe	Pro	Lys	Asn	Leu	Val
				165					170					175	
Gln	Ile	Lys	Ser	Asn	Lys	Asp	Lys	Glu	Gly	Lys	Val	Phe	Tyr	Ser	Ile
		180						185					190		
Thr	Gly	Gln	Gly	Ala	Asp	Thr	Pro	Pro	Val	Gly	Val	Phe	Ile	Ile	Glu
		195					200					205			
Arg	Glu	Thr	Gly	Trp	Leu	Lys	Val	Thr	Glu	Pro	Leu	Asp	Arg	Glu	Arg
	210					215					220				
Ile	Ala	Thr	Tyr	Thr	Leu	Phe	Ser	His	Ala	Val	Ser	Ser	Asn	Gly	Asn
225					230					235				240	
Ala	Val	Glu	Asp	Pro	Met	Glu	Ile	Leu	Ile	Thr	Val	Thr	Asp	Gln	Asn
			245					250					255		
Asp	Asn	Lys	Pro	Glu	Phe	Thr	Gln	Glu	Val	Phe	Lys	Gly	Ser	Val	Met
		260						265					270		
Glu	Gly	Ala	Leu	Pro	Gly	Thr	Ser	Val	Met	Glu	Val	Thr	Ala	Thr	Asp
		275					280					285			
Ala	Asp	Asp	Asp	Val	Asn	Thr	Tyr	Asn	Ala	Ala	Ile	Ala	Tyr	Thr	Ile
	290					295					300				

Leu Ser Gln Asp Pro Glu Leu Pro Asp Lys Asn Met Phe Thr Ile Asn
305 310 315 320

Arg Asn Thr Gly Val Ile Ser Val Val Thr Thr Gly Leu Asp Arg Glu
325 330 335

Ser Phe Pro Thr Tyr Thr Leu Val Val Gln Ala Ala Asp Leu Gln Gly
340 345 350

Glu Gly Leu Ser Thr Thr Ala Thr Ala Val Ile Thr Val Thr Asp Thr
355 360 365

Asn Asp Asn Pro Pro Ile Phe Asn Pro Thr Thr Tyr Lys Gly Gln Val
370 375 380

Pro Glu Asn Glu Ala Asn Val Val Ile Thr Thr Leu Lys Val Thr Asp
385 390 395 400

Ala Asp Ala Pro Asn Thr Pro Ala Trp Glu Ala Val Tyr Thr Ile Leu
405 410 415

Asn Asp Asp Gly Gly Gln Phe Val Val Thr Thr Asn Pro Val Asn Asn
420 425 430

Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala Lys Gln
435 440 445

Gln Tyr Ile Leu His Val Ala Val Thr Asn Val Val Pro Phe Glu Val
450 455 460

Ser Leu Thr Thr Ser Thr Ala Thr Val Thr Val Asp Val Leu Asp Val
465 470 475 480

Asn Glu Ala Pro Ile Phe Val Pro Pro Glu Lys Arg Val Glu Val Ser
485 490 495

Glu Asp Phe Gly Val Gly Gln Glu Ile Thr Ser Tyr Thr Ala Gln Glu
500 505 510

Pro Asp Thr Phe Met Glu Gln Lys Ile Thr Tyr Arg Ile Trp Arg Asp
515 520 525

Thr Ala Asn Trp Leu Glu Ile Asn Pro Asp Thr Gly Ala Ile Ser Thr
 530 535 540

Arg Ala Glu Leu Asp Arg Glu Asp Phe Glu His Val Lys Asn Ser Thr
 545 550 555 560

Tyr Thr Ala Leu Ile Ile Ala Thr Asp Asn Gly Ser Pro Val Ala Thr
 565 570 575

Gly Thr Gly Thr Leu Leu Leu Ile Leu Ser Asp Val Asn Asp Asn Ala
 580 585 590

Pro Ile Pro Glu Pro Arg Thr Ile Phe Phe Cys Glu Arg Asn Pro Lys
 595 600 605

Pro Gln Val Ile Asn Ile Ile Asp Ala Asp Leu Pro Pro Asn Thr Ser
 610 615 620

Pro Phe Thr Ala Glu Leu Thr His Gly Ala Ser Ala Asn Trp Thr Ile
 625 630 635 640

Gln Tyr Asn Asp Pro Thr Gln Glu Ser Ile Ile Leu Lys Pro Lys Met
 645 650 655

Ala Leu Glu Val Gly Asp Tyr Lys Ile Asn Leu Lys Leu Met Asp Asn
 660 665 670

Gln Asn Lys Asp Gln Val Thr Thr Leu Glu Val Ser Val Cys Asp Cys
 675 680 685

Glu Gly Ala Ala Gly Val Cys Arg Lys Ala Gln Pro Val Glu Ala Gly
 690 695 700

Leu Gln Ile Pro Ala Ile Leu Gly Ile Leu Gly Gly Ile Leu Ala Leu
 705 710 715 720

Leu Ile Leu Ile Leu Leu Leu Leu Leu Phe Leu Arg Arg Arg Ala Val
 725 730 735

Val Lys Glu Pro Leu Leu Pro Pro Glu Asp Asp Thr Arg Asp Asn Val
 740 745 750

Tyr Tyr Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp Phe Asp
755 760 765

Leu Ser Gln Leu His Arg Gly Leu Asp Ala Arg Pro Glu Val Thr Arg
770 775 780

Asn Asp Val Ala Pro Thr Leu Met Ser Val Pro Arg Tyr Leu Pro Arg
785 790 795 800

Pro Ala Asn Pro Asp Glu Ile Gly Asn Phe Ile Asp Glu Asn Leu Lys
805 810 815

Ala Ala Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Leu Val
820 825 830

Phe Asp Tyr Glu Gly Ser Gly Ser Glu Ala Ala Ser Leu Ser Ser Leu
835 840 845

Asn Ser Ser Glu Ser Asp Lys Asp Gln Asp Tyr Asp Tyr Leu Asn Glu
850 855 860

Trp Gly Asn Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu
865 870 875 880

Asp Asp

<210> 4
<211> 906
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(906)
<223> Alpha-1 Catenin, Swissprot Accession P35221

<400> 4

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Ser Leu Glu Ile Arg Thr Leu Ala Val Glu Arg Leu Leu Glu Pro Leu
20